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SEQUENCE LISTING

<110> Shewchuk, Lisa Marie
Hassell, Anne Moore
Brignola, Perry Scott

<120> ERB4 Co-Crystal

<130> PU4804USw

<140> US 10/543,046

<141> 2005-07-21

<150> PCT/US04/01291

<151> 2004-01-20

<150> US 60/441,443

<151> 2003-01-21

<160> 5

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 364

<212> PRT

<213> Homo sapein

<400> 1

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Val	Glu	Pro	Leu	Thr	Pro	Ser	Gly	Thr	Ala	Pro	Asn	Gln	Ala	Gln	Leu
			20					25					30		
Arg	Ile	Leu	Lys	Glu	Thr	Glu	Leu	Lys	Arg	Val	Lys	Val	Leu	Gly	Ser
		35					40				45				
Gly	Ala	Phe	Gly	Thr	Val	Tyr	Lys	Gly	Ile	Trp	Val	Pro	Glu	Gly	Glu
	50					55				60					
Thr	Val	Lys	Ile	Pro	Val	Ala	Ile	Lys	Ile	Leu	Asn	Glu	Thr	Thr	Gly
65					70				75					80	
Pro	Lys	Ala	Asn	Val	Glu	Phe	Met	Asp	Glu	Ala	Leu	Ile	Met	Ala	Ser
			85					90					95		
Met	Asp	His	Pro	His	Leu	Val	Arg	Leu	Gly	Val	Cys	Leu	Ser	Pro	
			100					105				110			
Thr	Ile	Gln	Leu	Val	Thr	Gln	Leu	Met	Pro	His	Gly	Cys	Leu	Leu	Glu
		115					120					125			
Tyr	Val	His	Glu	His	Lys	Asp	Asn	Ile	Gly	Ser	Gln	Leu	Leu	Leu	Asn
	130					135					140				
Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met	Met	Tyr	Leu	Glu	Glu	Arg	Arg
145					150				155					160	
Leu	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro
			165						170					175	
Asn	His	Val	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Ala	Arg	Leu	Leu	Glu	Gly
			180				185					190			
Asp	Glu	Lys	Glu	Tyr	Asn	Ala	Asp	Gly	Gly	Lys	Met	Pro	Ile	Lys	Trp
		195					200					205			
Met	Ala	Leu	Glu	Cys	Ile	His	Tyr	Arg	Lys	Phe	Thr	His	Gln	Ser	Asp
	210					215					220				
Val	Trp	Ser	Tyr	Gly	Val	Thr	Ile	Trp	Glu	Leu	Met	Thr	Phe	Gly	Gly
225					230					235				240	
Lys	Pro	Tyr	Asp	Gly	Ile	Pro	Thr	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu
			245						250				255		

SEQLIST

Lys Gly Glu Arg Leu Pro Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr
 260 265 270
 Met Val Met Val Lys Cys Trp Met Ile Asp Ala Asp Ser Arg Pro Lys
 275 280 285
 Phe Lys Glu Leu Ala Ala Glu Phe Ser Arg Met Ala Arg Asp Pro Gln
 290 295 300
 Arg Tyr Leu Val Ile Gln Gly Asp Asp Arg Met Lys Leu Pro Ser Pro
 305 310 315 320
 Asn Asp Ser Lys Phe Phe Gln Asn Leu Leu Asp Glu Glu Asp Leu Glu
 325 330 335
 Asp Met Met Asp Ala Glu Glu Tyr Leu Val Pro Gln Ala Phe Asn Ile
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 355 360

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 <212> DNA
 <213> Homo sapien

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 aagagggttaa aagtccttgg ctcagggtgct tttggaacgg tttataaagg tatttgggta 180
 cctgaaggag aaactgtgaa gattcctgtg gctattaaga ttcttaatga gacaactggg 240
 cccaaggcaa atgtggagtt catggatgaa gctctgatca tggcaagtat ggatcatcca 300
 cacctagtcg gggtgctggg tgtgtgtctg agcccaacca tccagctggg tactcaactt 360
 atgccccatg gctgcctgtt ggagtatgtc cagcagcaca aggataacat tggatcacaa 420
 ctgctgctta actgggtgtg ccagatagct aagggaatga tgtacctgga agaaagacga 480
 ctgcttcacg gggatttggc agcccgtaat gtcttagtga aatctccaaa ccatgtgaaa 540
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 ggaggaaaga tgccaattaa atggatggct ctggagtgtg tacattacag gaaattcacc 660
 catcagagtg acgtttggag ctatggagtt actatatggg aactgatgac ctttggagga 720
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<210> 3
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 <213> Artificial Sequence

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 <223> ErbB4 amino acid positions for which structural coordinates are shown in Table 2

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 20 25 30
 Gly Thr Val Tyr Lys Gly Ile Trp Val Pro Ala Gly Glu Ala Val Lys
 35 40 45
 Ile Pro Val Ala Ile Lys Ile Ala Val Ala Asn Val Glu Phe Met Asp
 50 55 60
 Glu Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu Val Arg Leu
 65 70 75 80
 Leu Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr Gln Leu Met
 85 90 95
 Pro His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys Asp Asn Ile
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Gly	Ser	Gln	Leu	Leu	Leu	Asn	Trp	Cys	Val	Gln	Ile	Ala	Lys	Gly	Met
Met	Tyr	115	Glu	Glu	Arg	Arg	120	Leu	Val	His	Arg	Asp	125	Leu	Ala
130	Val	Leu	Val	Lys	Ser	Pro	135	Ala	His	Val	Lys	140	Ile	Thr	Asp
145	Ala	Arg	Leu	Leu	Glu	Gly	150	Asp	Glu	Lys	Glu	155	Tyr	Asn	Ala
160	Gly	Lys	Met	Pro	Ile	Lys	165	Trp	Met	Ala	Leu	170	Glu	Cys	Ile
175	Ala	Phe	Thr	His	Gln	Ser	180	Val	Trp	Ser	Tyr	185	Gly	Val	His
190	Glu	Leu	Met	Thr	Phe	Gly	195	Gly	Lys	Pro	Tyr	200	Asp	Gly	Ile
205	210	Ile	Pro	Asp	Leu	Leu	215	Glu	Lys	Gly	Glu	220	Arg	Leu	Pro
225	Ile	Cys	Thr	Ile	Asp	Val	230	Tyr	Met	Val	Met	235	Val	Lys	Cys
240	245	Asp	Ala	Asp	Ser	Arg	250	Pro	Lys	Phe	Ala	255	Glu	Leu	Ala
260	Arg	Met	Ala	Arg	Asp	Pro	265	Gln	Arg	Tyr	Leu	270	Val	Ile	Gln
275	Ala	Ala	Ala	Ala	Pro	Leu	280	Thr	Pro	Ser	Gly	285	Thr	Ala	Pro
290	Gln	Leu	Arg	Ile	Leu	Ala	295	Glu	Thr	Glu	Leu	300	Arg	Val	Ala
305	Gly	Ser	Gly	Ala	Phe	Gly	310	Thr	Val	Tyr	Lys	315	Gly	Ile	Trp
320	325	Glu	Ala	Val	Ala	Ile	330	Pro	Val	Ala	Ile	335	Lys	Ile	Ala
340	Asn	Val	Ala	Phe	Met	Asp	345	Glu	Ala	Leu	Ile	350	Met	Ala	Ser
355	Pro	His	Leu	Val	Arg	Leu	360	Gly	Val	Cys	Leu	365	Ser	Pro	Thr
370	Leu	Val	Thr	Gln	Leu	Met	375	Pro	His	Gly	Cys	380	Leu	Leu	Glu
385	Glu	His	Lys	Asp	Asn	Ile	390	Gly	Ser	Gln	Leu	395	Leu	Leu	Asn
400	Gln	Ile	Ala	Lys	Gly	Met	405	Met	Tyr	Leu	Glu	410	Glu	Arg	Arg
415	Arg	Asp	Leu	Ala	Ala	Arg	420	Asn	Val	Leu	Val	425	Lys	Ser	Pro
430	Lys	Ile	Thr	Asp	Phe	Gly	435	Leu	Ala	Arg	Leu	440	Leu	Glu	Gly
445	Ala	Tyr	Asn	Ala	Asp	Gly	450	Gly	Ala	Met	Pro	455	Ile	Lys	Trp
460	Glu	Cys	Ile	His	Tyr	Arg	465	Ala	Phe	Thr	His	470	Gln	Ser	Asp
475	Tyr	Gly	Val	Thr	Ile	Trp	480	Glu	Leu	Met	Thr	485	Phe	Gly	Lys
490	Gly	Ile	Pro	Thr	Ala	Glu	495	Ile	Pro	Asp	Leu	500	Leu	Glu	Lys
505	Leu	Pro	Gln	Pro	Pro	Ile	510	Cys	Thr	Ile	Asp	515	Val	Tyr	Met
520	Lys	Cys	Trp	Met	Ile	Asp	525	Ala	Asp	Ser	Arg	530	Lys	Phe	Ala
535	Ala	Ala	Glu	Phe	Ser	Arg	540	Met	Ala	Arg	Asp	545	Pro	Gln	Arg
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 <211> 11
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 <213> Artificial Sequence

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 <223> His tag for Erb4 cytoplasmic domain

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<210> 5
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Substrate peptide for Erb4 activity assay

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